I. AMENDMENTS TO THE SPECIFICATION

Please delete the Sequence Listing previously submitted in its entirety and replace it with the Sequence Listing submitted herewith.

Paragraph on page 4, lines 6 to 12:

The present invention, in one aspect, provides an isolated nucleic acid molecule comprising a nucleotide sequence or complement thereof, wherein the nucleotide sequence encodes an *ANT*-like polypeptide having in the N-terminal to C-terminal direction two AP2 DNA binding domains followed in the C-terminal by an amino acid subsequence selected from the group consisting of Xaa-Ser-Ser-Ser-Arg-Glu (SEQ ID NO: 25), Xaa-Ser-Asn-Ser-Arg-Glu (SEQ ID NO: 26), and Asn-Ser-Ser-Ser-Arg-Asn (SEQ ID NO: 27), wherein Xaa is an amino acid residue having an aliphatic side chain and selected from the group consisting of Gly, Ala, Val, Leu, and Ile.

Paragraph on page 5, lines 18 to 28:

The present invention, in another aspect, provides a substantially purified polypeptide the amino acid sequence of which: (1) comprises in the N-terminal to C-terminal direction two AP2 DNA binding domains followed in the C-terminal by an amino acid subsequence selected from group consisting of Xaa-Ser-Ser-Ser-Arg-Glu (SEQ ID NO: 25), Xaa-Ser-Asn-Ser-Arg-Glu (SEQ ID NO: 26), and Asn-Ser-Ser-Ser-Arg-Asn (SEQ ID NO: 27), wherein Xaa is an amino acid residue having an aliphatic side chain and selected from the group consisting of Gly, Ala, Val, Leu, and Ile; (2) is encoded by a first nucleotide sequence which specifically hybridizes under stringent conditions to the complement of a second nucleotide sequence selected from the

groups consisting of SEQ ID NO: 1, 3, 5, 7, 8, 10, and 12; (3) is encoded by a third nucleotide sequence that has at least 60% sequence identity to a member selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 8, 10, and 12; or (4) has at least 60% sequence identity to a member selected from the group consisting of SEQ ID Nos: 2, 4, 6, 9, 11, and 13.

Paragraph on page 6, lines 6 to 29:

The present invention also provides a method for increasing the size of one or more plant organs of a plant by expressing ectopically a nucleic acid molecule that encode a polypeptide the amino acid sequence of which has at least 60% sequence identity to a member selected from the group consisting of SEQ ID NOs: 2, 4, 6, 9, 11, and 13 or comprises in the N-terminal to C-terminal direction two AP2 DNA binding domains followed in the C-terminal by an amino acid subsequence selected from group consisting of Xaa-Ser-Ser-Ser-Arg-Glu (SEQ ID NO: 25), Xaa-Ser-Asn-Ser-Arg-Glu (SEQ ID NO: 26), and Asn-Ser-Ser-Ser-Arg-Asn (SEQ ID NO: 27), wherein Xaa is an amino acid residue having an aliphatic side chain and selected from the group consisting of Gly, Ala, Val, Leu, and Ile. The method of the present invention for increasing the size of one or more plant organs of a plant comprises the steps of: (a) inserting into the genome of a plant an exogenous nucleic acid molecule comprising in the 5' to 3' direction and operably linked, (i) a promoter that functions in the cells of a selected plant tissue, (ii) a structural nucleotide sequence that causes the production of an *ANT*-like polypeptide the amino acid sequence of which has at least 60% sequence identity to a member selected from the group consisting of SEQ ID Nos: 2, 4, 6, 9, 11, and 13, or comprises in the N-terminal to C-terminal direction two AP2 DNA binding domains followed in the C-terminal by an amino acid subsequence selected from group consisting of Xaa-Ser-Ser-Ser-Arg-Glu (SEQ ID NO: 25),

Xaa-Ser-Asn-Ser-Arg-Glu (SEQ ID NO: 26), and Asn-Ser-Ser-Ser-Arg-Asn (SEQ ID NO: 27), wherein Xaa is an amino acid residue having an aliphatic side chain and selected from the group consisting of Gly, Ala, Val, Leu, and Ile, and (iii) a 3' non-translated nucleotide sequence that functions in plant cells to cause transcriptional termination and the addition of polyadenylated nucleotides to the 3' end of a RNA sequence; (b) obtaining transformed plant cells containing the exogenous nucleic acid molecule of step (a); and (c) regenerating from the transformed plant cells a transformed plant that ectopically expresses the *ANT*-like polypeptide in the plant cells. The exogenous nucleic acid molecule may optionally include introns, 5' untranslated leader sequences or other nucleotide sequences designed to enhance transcription and/or translation.

Paragraph on page 7, lines 10 to 14:

Figure 1 shows a comparison of the amino acid sequences of the *Arabidopsis ANT* and two soybean *ANT*-like polypeptides. The amino acid sequences were aligned using Window32 MegAlign™ 4.00 expert sequence analysis software from DNASTAR, Inc. (Madison, WI) using the set of default parameters (Gap Penalty: 11; Gap Length Penalty: 3; Ktuple: 2), based on Hein's method (Hein, Methods Mol. Biol. 25:349-364 (1994)) (SEQ ID NOS 2, 4 & 34 are disclosed respectively in order of appearance).

Paragraph on page 7, lines 15 to 16:

Figure 2 shows a comparison of the amino acid sequences of the *Arabidopsis ANT* and soybean, rice, cotton and corn *ANT*-like polypeptides (g1244708 disclosed as residues 1-551 of SEQ ID NO: 34; GmANT1 disclosed as residues 1-659 of SEQ ID NO: 2; OsANT1 disclosed as residues 1-665 of SEQ ID NO: 9; GhANT1 disclosed as residues

1-582 of SEQ ID NO: 11; ZmANT1 disclosed as residues 6-251 of SEQ ID NO: 13; GmANT2 disclosed as residues 1-661 of SEQ ID NO: 4; OsANT1 disclosed as residues 1-638 of SEQ ID NO: 6).

Paragraph on page 10, line 12 to page 11, line 7:

One aspect of the present invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence or complement thereof, wherein the nucleotide sequence encodes a polypeptide having in the N-terminal to C-terminal direction two AP2 DNA binding domains followed in the C-terminal by an amino acid subsequence selected from group consisting of Xaa-Ser-Ser-Ser-Arg-Glu (SEQ ID NO: 25), Xaa-Ser-Asn-Ser-Arg-Glu (SEQ ID NO: 26), and Asn-Ser-Ser-Ser-Arg-Asn (SEQ ID NO: 27), wherein Xaa is an amino acid residue having an aliphatic side chain and selected from the group consisting of Gly, Ala, Val, Leu, and Ile. In a preferred embodiment, the amino acid subsequence is selected from the group consisting of Ser-Ser-Leu-Xaa-Thr-Ser-Xaa-Ser-Ser-Ser-Arg-Glu (SEQ ID NO: 28), Ser-Ser-Leu-Xaa-Pro-Ser-Xaa-Ser-Asn-Ser-Arg-Glu (SEQ ID NO: 29), Ser-Ser-Leu-Xaa-Thr-Ser-Xaa-Ser-Asn-Ser-Arg-Glu (SEQ ID NO: 30), and Ser-Leu-Xaa-Asn-Ser-Ser-Ser-Arg-Asn (SEQ ID NO: 31). In a particular preferred embodiment, the polypeptide of the present invention further comprises a second amino acid subsequence selected from the group consisting of Leu-Gly-Phe-Ser-Leu-Ser (SEQ ID NO: 35), Leu-Gly-Phe-Ser-Leu-Thr (SEQ ID NO: 36), Met-Pro-Leu-Lys-Ser-Asp-Gly-Ser (SEQ ID NO: 37), Met-Pro-Leu-Arg-Ser-Asp-Gly-Ser (SEQ ID NO: 38), Met-Pro-Ile-Lys-Ser-Asp-Gly-Ser (SEQ ID NO: 39), Pro-Lys-Leu-Glu-Asp-Phe (SEQ ID NO: 40), and Pro-Lys-Val-Glu-Asp-Phe (SEQ ID NO: 41).

Paragraph on page 36, line 28 to page 37, line 10:

The present invention, in another aspect, provides a substantially purified polypeptide the amino acid sequence of which comprises in the N-terminal to C-terminal direction two AP2 DNA binding domains followed in the C-terminal by an amino acid subsequence selected from group consisting of Xaa-Ser-Ser-Ser-Arg-Glu (SEQ ID NO: 25), Xaa-Ser-Asn-Ser-Arg-Glu (SEQ ID NO: 26), and Asn-Ser-Ser-Ser-Arg-Asn (SEQ ID NO: 27), preferably selected from the group consisting of Ser-Ser-Leu-Xaa-Thr-Ser-Xaa-Ser-Ser-Ser-Arg-Glu (SEQ ID NO: 28), Ser-Ser-Leu-Xaa-Pro-Ser-Xaa-Ser-Asn-Ser-Arg-Glu (SEQ ID NO: 29), Ser-Ser-Leu-Xaa-Thr-Ser-Xaa-Ser-Asn-Ser-Arg-Glu (SEQ ID NO: 30), and Ser-Leu-Xaa-Asn-Ser-Ser-Ser-Arg-Asn (SEQ ID NO: 31) wherein Xaa is an amino acid residue having an aliphatic side chain and selected from the group consisting of Gly, Ala, Val, Leu, and Ile. In a particular preferred embodiment, the substantially purified polypeptide of the present invention further comprises a second amino acid subsequence selected from the group consisting of Leu-Gly-Phe-Ser-Leu-Ser (SEQ ID NO: 35), Leu-Gly-Phe-Ser-Leu-Thr (SEQ ID NO: 36), Met-Pro-Leu-Lys-Ser-Asp-Gly-Ser (SEQ ID NO: 37), Met-Pro-Leu-Arg-Ser-Asp-Gly-Ser (SEQ ID NO: 38), Met-Pro-Ile-Lys-Ser-Asp-Gly-Ser (SEQ ID NO: 39), Pro-Lys-Leu-Glu-Asp-Phe (SEQ ID NO: 40), and Pro-Lys-Val-Glu-Asp-Phe (SEQ ID NO: 41). In some groups of amino acids, the side chains are described as having aliphatic side chains. Aliphatic side chains are often designated as a side chain of organic chemical compounds in which the carbon atoms are linked in open chains, for example Gly, Ala, Val, Leu, and Ile.

Paragraph on page 58, lines 21 to 31:

To clone *ANT* into an expression vector, the *ANT* coding sequence from a clone was released from the TA vector by digesting with *EcoRI* and *SalI*. This linear DNA segment was then religated to the binary vector pMON23435, that had been linearized by *EcoRI* and *XhoI*, using T4 DNA ligase (BRL/Life Technologies, Inc., Gainthersburg, Md.). The ligation reaction was performed according to the manufacturer's instruction. The resulting plasmid was confirmed by restriction mapping (for example, see Griffiths, et al, *An Introduction to Genetic Analysis*, 6^{th} *Edition* pp 449-451, ISBN 0-7167-2604-1, W.H. Freeman and Co., New York) and sequencing. As the chosen *EcoRI-XhoI* cloning site in the vector was flanked by a CaMV e35S promoter at the upstream (5') and an epitope tag (Flag, which encodes the oligo peptide DYKDDDK (SEQ ID NO: 42), SIGMA, St Louis) at the downstream (3'), the *Arabidopsis ANT* in this construct is thus tagged at the C-terminus by the Flag epitope tag and will be driven transcriptionally by the CaMV e35S promoter upon transformation in *Arabidopsis*.